assigned to new sequences as they are identified. Lists of such new names will be published in the following WHO Nomenclature Report.

AUTHOR CONTRIBUTIONS

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CONFLICT OF INTEREST

The authors confirm that there are no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions. The sequence is freely available in the IPD-IMGT/HLA Database.

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Characterization of the novel *HLA-DQA1*05:05:14* allele by sequencing-based typing

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*HLA-DQA1*05:05:14* differs from *HLA-DQA1*05:05:01:04* by one nucleotide substitution in codon −8 in exon 1.

KEYWORDS

HLA, *HLA-DQA1*05:05:14*, novel allele, sequencing-based typing

We report here a novel *HLA-DQA1*05:05* allele, now named *DQA1*05:05:14* that carries one nucleotide substitution in exon 1 when compared to the *DQA1*05:05:01:04* allele, identified in a volunteer bone

```
AA Codon                    -20                 -15                 -10                  -5                   1
DQA1*05:05:01:04   ATG ATC CTA AAC AAA GCT CTG ATG CTG GGG ACC CTT GCC CTG ACC ACC GTG ATG AGC CCC TGT GGA GGT GAA GAC
DQA1*05:05:14      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --T --- --- --- --- --- --- --- --- ---

AA Codon
DQA1*05:05:01:04   ATT GTG G
DQA1*05:05:14      --- --- -
```

FIGURE 1 Alignment of the sequence of exon 1 of *HLA-DQA1*05:05:14* with the sequence of *HLA-DQA1*05:05:01:04*. Dashes indicate nucleotide identity with the *HLA-DQA1*05:05:01:04* allele. Numbers above the sequence indicate codon position.

marrow donor. The HLA typing was performed using Next Generation Sequencing (AllType NGS, One Lambda, Canoga Park, CA) on the Ion S5 system platform (ThermoFisher Scientific, Waltham, MA),[1] from exons 1 to 4. The reads were analyzed using the TypeStream Visual Software version 2.1 (One Lambda). This donor was found to have a new *DQA1*05:05* allele and was consequently typed *A*02:01*, *32:01*; *B*14:02*, *44:02*; *C*02:02*, *07:04*; *DRB1*11:01*, *11:01*; *DRB3*02:02*, *02:02*; *DQA1*05:05:01*, *05:05:14*; *DQB1*03:01P*, *03:01P*; *DPA1*01:03*, *01:03*; *DPB1*02:01*, *04:02*. Using the IPD-IMGT/HLA Database,[2] nucleotide sequence alignment with HLA-DQA1 alleles shows that this new allele has one nucleotide change from *DQA1*05:05:01:04* in codon −8 in exon 1, where C → T, (ACC → ACT, Figure 1), not resulting in a coding change. This nucleotide change was confirmed by performing the typing twice in two different laboratories. We were confident in the phasing as the sample displayed a mean read length of 332 base pairs over all the loci, the mismatched A base was attributed 76 times to the new *HLA-DQA1*05:05*. The nucleotide sequence of the exons 1–4 of the new allele has been submitted to the GenBank database (Accession No. OP393478) and to the IPD-IMGT/HLA Database (Submission No. HWS10062886). The name *DQA1*05:05:14* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in September 2022. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,[3] names will be assigned to new sequences as they are identified. Lists of such new names will be published in the following WHO Nomenclature Report.

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